SEQUENCE LISTING

- (1) GENERAL INFORMATION
 - (i) APPLICANT: Horwath, K. L., et al.
 - (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
 - (iii) NUMBER OF SEQUENCES: 48
 - (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Dr. Kathleen L. Horwath
 - (B) STREET: Department of Biological Sciences, Binghamton University
 - (C) CITY: Binghamton
 - (D) STATE: New York
 - (E) ZIP: 13902-6000
 - (v) COMPUTER READABLE FORM
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 - (B) COMPUTER: IBM AT/ATX compatible
 - (C) OPERATING SYSTEM: Windows 95/98
 - (D)SOFTWARE: Microsoft Word
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: 60210446
 - (B) FILING DATE: June 8, 2000
 - (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: Mark Levy, Attorney-at-Law
 - (B) REGISTRATION NUMBER: 29-188
 - (C) REFERENCE/DOCKET NUMBER: RB125
 - (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: 607-722-6600
 - (B) TELEFAX: 607-724-2207

- (2) INFORMATION FOR SEQ. ID NO: 1
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Peptide
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) FRAGMENT TYPE: N-terminal fragment
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) (ELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE:
 - (ix) FEATURES:
 - (D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.86
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val 10 15

(2)	() () ()	i) S ii) iii) iv) vi)	(B) (C) (D) MOLE HYP ANTI- ORIG (A) (B) (C) IMMI	NCE LENGE TYPO STR. TOP CULE OTHE COLL ORG. IND. CEL IND.	CHAR. GTH: E: n: CHANDE: OLOG: TICAI TICAI SE: I SOUI ANISI IVIDI L TYI RARY	ACTEI 566 UC1e UC1e VE: C C C C C C C C C C C C C C C C C C C	RIST: base ic ac ic ac ic ac ic ac inea inea inea inea inea inea inea inea	ICS: e pa: cid ouble r to ml	e RNA moli non		le o	∽gan	ism			
(B) CLONE: 13.17 (ix)FEATURES (D) OTHER INFORMATION: Non-his-tagged, signal plus (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: GTGGATCCAA AGAATTCGGC ACGAGACTAC TAAG ATG AAG TTG CTC																
	G'	TGGA	TCCA	A AG	4 A T T (CGGC	ACG	AGAC'	TAC '	TAAG			TT <i>G</i> Leu			36
			ATC Ile												!	81
ACC Thr	GAG Glu	GCA Ala	CAA Gln 5	ATT Ile	GAG Glu	AAA Lys	CTG Leu	AAC Asn 10	AAG Lys	ATC Ile	AGC Ser	AAA Lys	AAA Lys 15	TGT Cys	1	26
CAA Gln	AAT Asn	GAA Glu	TDA Ser 20	GGA Gly	GTG Val	TCG Ser	CAA Gln	GAG Glu 25	ATC Ile	ATA Ile	ACC Thr	AAA Lys	GCT Ala 30	CGC Arg	1	71
AAC Asn	GGT Gly	GAC Asp	TGG Trp 35	GAG Glu	GAC Asp	GAT Asp	CCT Pro	AAA Lys 40	CTG Leu	AAA Lys	CGC Arg	CAA Gln	GTT Val 45	TTT Phe	2.	<u> </u>
Cys	Val	GCC Ala	AGG Arg 50	Asn	Ala	Gly	Leu	Ala	Thr	GAA Glu	Ser	Gly	Glu	Val	2	ЬЪ
GTG Val	GTC Val	GAC Asp	GTG Val 65	TT6 Leu	AGG Arg	GAG Glu	AAG Lys	GTG Val 70	AGG Arg	AAG Lys	GTC Val	ACT Thr	GAC Asp 75	AAC Asn	3	06
GAC Asp	GAA Glu	GAA Glu	ACT Thr 80	GAG Glu	AAA Lys	ATC Ile	ATC Ile	AAT Asn 85	AAG Lys	TGC Cys	GCC Ala	GTC Val	AAG Lys 90	AGA Arg	3.	51
GAT Asp	ACT Thr	GTT Val	GAA Glu 95	GAG Glu	ACG Thr	GTG Val	TTC Phe	AAT Asn 100	ACT Thr	TTC Phe	AAA Lys	TGT Cys	GTC Val 105	ATG Met	3'	96
			CCA Pro 110								ACCA	ACCA(EGA		4:	39
CTAG	TAGA	ATG I	GTTCA	AAT	56 T	STGC	ГТТА	CATA	ATAAA	T A A A	AAA	STGT	ГТС		4	89
TGAT	GTA	444	A A A A	AAAA	AA AA	AAA	AAAA	4 AA(TCGA	AGAG	TAT	ГСТА	SAG		5	37
CGGC	CGC	SGG (CCCAT	CGT	TT T	CAC	C								51	56

- (2) INFORMATION FOR SEQ. ID NO: 3
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13-17
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Precursor Protein for Tm 13.17
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
- Met Lys Leu Leu Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val -15 -10 -5
- Gln Ala Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys
- Lys Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala 15 20 25 30
- Arg Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe 35 40 45
- Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val
 50 55 60
- Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu 65 70 75
- Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val 80 85 90
- Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro 95 100 105 110
- Lys Phe Ser Pro Val Asp * 115

- (2) INFORMATION FOR SEQ. ID NO: 4
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Mature Protein for Tm 13.17
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
- Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys 10 15
- Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn 20 25 30
- Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val 35 40 45
- Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp 50 55 60
- Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr 65 70 75 80
- Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu 85 90 95
- Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe
- Ser Pro Val Asp *

(2)	(i (li)	CQUEN (A) (B) (C) (D) (D) (ANTI- (B) (A) (C) IMME (A) (B) (A) (B) (CD)	ICE (LENG TYPE STRA TOP(IULE)THE1 -SENS INAL ORGA IND1 CELL IDIA1 CLON CES OTHE	CHARA TH: C: nu NDEI LOGY TYPE CICAL SE: r SOUF NISN CVIDU CRARY: RE: G	ACTER 481 uclei NESS Y: li I: cI I: no RCE: 1: Te DURCE I: cDN I: CN RCE	enebi ISOLA Tat b I:	CCS: pai id ouble compa TE: body	RNA nolit none and	≗ who] His-t	agge	_		al pl	us
GGC	ACGAO	GCA A				eu L	TC T _eu L -15				\la F				46
							CTC Leu l								97
							TGC Cys								136
							CGC Arg								181
							CTC Leu								556
		Thr	Glu	Ala	Gly	Asp	ACC Thr	Asn	Val	Glu	Val				271
							GAC Asp								376
							GCC Ala								367
							GAC Asp								406
	GAT Asp 115		TTG	F TTT(STA '	ΓΤΤ <i>GI</i>	4CTG∤	AA T'	ΓΤΤΕ	ACAA	ΓΑΑ	AGGT <i>i</i>	AATA		455

TCGTTATGTA AAAAAAAAA AAAAAA

(2)	(i (i (i (v	i) M ii) M ii) V v) A vi) O	QUEN (A) (C) (D) (OLEC HYPO RIGI (B) (C) IMME (A) (B) (ATUR (D)	CE CLONGES	HARA TH: NDED LOGY TYPE ICAL ESOUR VIDU TYPE EXOR VIDU EXOR IE: IR IN	CTER 482 clei NESS : li : cD co CE: Fell URCE CDN 153	ISTI base c ac near NA t 20LA at b 1ATIO	CS: pai id uble o mR	NA nolit none and	whol	agge			al pl	us
GGCA	CGAG	SCA A	A A A /	TG A let L	AA C .ys L	.eu L	TC T .eu L -15	TG T .eu (GC 1 Sys F	TTT 6	la F	TTC 0 he A -10	SCC @ Nla #	SCC Ala	46
		ATC Ile -5													71
Arg	AAC Asn 10	AAG Lys	ATC Ile	Ser Ser	AAA Lys	GAA Glu 15	TGC Cys	CAG Gln	CAG Gln	GTG Val	Zer 20	GGA Gly	GTG Val	TCC Ser	136
Gln		ACG Thr													181
		ATG Met													556
GTG Val	Ala	ACC Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	CTC Leu	AAA Lys	GCC Ala	271
		AAG Lys													316
CAG Gln	AAG Lys 85	TGC Cys	GTG Val	GTC Val	AAG Lys	AAG Lys 90	GCC Ala	ACA Thr	CCA Pro	GAG Glu	GAA Glu 95	ACG Thr	GCT Ala	TAT Tyr	361
Asp	Thr 100	TTC Phe	Lys	Cys	Ile	Tyr 105	Asp	Ser	Lys	Pro	Asp Դյը	Phe	Ser	Pro	406
ATT		T A A *	TTG'	TTTT(GTA '	TTTG,	ACTG,	AA T	TTTG.	ACAA'	Г АА.	AGGT.	ACTA		455

TCGTTATGAA AAAAAAAAA AAAAAA

- (2) INFORMATION FOR SEQ. ID NO: 7
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, and 7.5
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Precursor Protein for Tm 12.84
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
- Met Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
 -15 -5
- Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
- Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val 15 20 25 30
- Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu 35 40 45
- Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60
- Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu 65 70 75
- Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu 80 85 90
- Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 100 105

- (2) INFORMATION FOR SEQ. ID NO: 8
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, and 7.5
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Mature Protein for Tm 12.84
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
- Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys

 5 10 15
- Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr 20 25 30
- Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe 35 40 45
- Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu 50 55 60
- Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp 65 70 75 80
- Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr 85 90 95
- Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
- Pro Ile Asp *

(2) INFORMATION FOR SEQ. ID NO: 9 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 4&L base pairs (B) TYPE: nuclEic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 3.4 (ix)FEATURES (D) OTHER INFORMATION: Non-His-tagged, Signal plus (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC Met Lys Leu Leu Cys Phe Ala Phe Ala Ala -15 -10	46
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys -5	91
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC l Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser LO L5 20	136
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT l Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35	181
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA F Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly 4D 45 50	55P
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC a Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala 55 60	271
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val 70 75 80	31F
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT G Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr 85 90 95	361
GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro 100 105 110	40b
ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA Ile Asp * 115	455

TCGTTATGTA AAAAAAAAA AAAAA

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(2) INFORMATION FOR SEQ. ID NO: 10
(i) SEQUENCE CHARACTERISTICS:
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- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
- (ix)FEATURES
- (D) OTHER INFORMATION: Precursor Protein for Clone 3.4
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
-15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu AD 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp 95 100 105

- (2) INFORMATION FOR SEQ. ID NO: 11
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Mature Protein for Clone 3.4
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
- Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys 1 10 15
- Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr 20 25 30
- Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
 35 40 45
- Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu 50 55 60
- Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp 65 70 75 80
- Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
 85 90 95
- Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser L00 L05 L10
- Pro Ile Asp *

(2) INFORMATION FOR SEQ. ID NO: 12 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 482 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 3.9 (ix)FEATURES (D) OTHER INFORMATION: Non-His-tagged, Signal plus (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:												
GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC Met Lys Leu Leu Cys Phe Ala Phe Ala Ala -15 -10	Ь											
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA 9 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys -5 1 5	l											
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC l3 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser l0 l5 20	Ь											
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT 186 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35	1											
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA 22 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly 40 45 50	Ь											
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC 27 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala 55 60 65	ь											
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG 3L Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val 70 75 80	Ь											
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 36 Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr 85 90	1											
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 40 Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro 100 105 110	Ь											
ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA 45 Ile Asp * 115	5											

TCGTTATGAA AAAAAAAAA AAAAAAA

- (2) INFORMATION FOR SEQ. ID NO: 13
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Precursor Protein for Clone 3.9
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
- Met Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5
- Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
- Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val 15 20 25 30
- Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu 35 40 45
- Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60
- Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu 65 70 75
- Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu 80 90
- Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp 95 100 105

- (2) INFORMATION FOR SEQ. ID NO: 14
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: ⊂DNA
 - (B) CLONE: 3.9
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Mature protein for Clone 3.9 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
- Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys

 5
 10
 15
- Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr 20 25 30
- Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe 35 40 45
- Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu 50 55 60
- Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu Val Asp 65 70 75 80
- Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr 85 ′ 90 95
- Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
- Pro Ile Asp * 115

(2) INFORMATION FOR SEQ. ID NO: 15 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 481 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 7.5 (ix)FEATURES (D) OTHER INFORMATION: Non-his-tagged Signal plus (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:													
GGCACGAGCA			TGC TTT GCG T Cys Phe Ala F		46								
			GAC GAA CAG Asp Glu Gln 5		90								
			G CAG GTG TCC n Gln Val Ser 20		73P								
			A GGT GTC TTG Gly Val Leu 35		181								
			TTC TCG AAG s Phe Ser Lys 50		556								
			r GTG GAG GTA n Val Glu Val 65		271								
			A GAG GTG GAC u Glu Val Asp BO		376								
			A CCA GAG GAA r Pro Glu Glu 95		361								
			T AAA CCT GAT r Lys Pro Asp 110		406								
ATT GAT TAA Ile Asp * 115	A TTGTTTTGTA	TTTGGCTGAA	TTTTGACAAT AA	AGGTACTA	455								

TCGTTATGTA AAAAAAAAA AAAAA

- (2) INFORMATION FOR SEQ. ID NO: 16
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
 - (ix)FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	186
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -5	537
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser L	276
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	321
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 3D 35 4D	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 50 55	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 110 115	595
TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

- (2) INFORMATION FOR SEQ. ID NO: 17
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: ⊂DNA
 - (B) CLONE: 2.2
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30
- Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala -25 -20 -15
- Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile -10 -5 5
- Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
- Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35
- Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val 40 45 50
- Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu 55 60 65 70
- Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
 75 80 85
- Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 95 100
- Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 115

(2) INFORMATION FOR SEQ. ID NO: 18 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 2.2 (ix)FEATURES (D) OTHER INFORMATION: His-tagged; signal minus (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -30 -25	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -20 -15 -10	141
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln -5	186
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val 10 15 20	537
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp 25 30 35	276
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr 40 45 50	357
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys 55 60	366
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile 70 75 80	411
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala 85 90 95	45Ь
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser 100	50l
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT Pro Ile Asp * 115	543

- (2) INFORMATION FOR SEQ. ID NO: 19
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Mature Protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5
- Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val 15 20 25 30
- Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu 35 40 45
- Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn 50 55 60
- Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu 65 70 75
- Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu 80 85 90
- Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp ዓ5 100 105 110
- Phe Ser Pro Ile Asp *

- (2) INFORMATION FOR SEQ. ID NO: 20
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
 - (ix)FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal Plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG													50		
AAG	SAGA1	TAT A		ATG (Met (Ser S					lis H				96
				CCG Pro											141
				GGT Gly											186
				TGC Cys											537
				GAC Asp											276
				CAG Gln											357
				GGT Gly											366
				TTC Phe											411
				GTG Val											456
				GAA Glu											501
				CCA Pro											546
		Asp		AAA Lys									TTG	TTTTGTA	595
ттт	GACT	GAA	тттт	GACA.	АТ А	AAGG'	TACT.	A TC	GTTA	TGAA	AAA	AAAA.	AAA		645

P85

AAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT

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(2) INFORMATION FOR SEQ. ID NO: 21
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
- (ix)FEATURES
- (D) OTHER INFORMATION: Precursor Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30
- Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala -25 -20 -15
- Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
- Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
- Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35
- Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val 40 45 50
- Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu 55 60 65 70
- Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys 75 80 85
- Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys 90 95 100
- Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 115

(2)	(i (i (i (v	i) SE ii) N iii) iv) / /ii) (x) FE	(A) (B) (C) (D) (D) 10LE(HYP(ANTI- (A) (B) (C) IMME (A) (B) (B)	NCE (LENG TYPE STRA TOP(CULE OTHET SINAL ORGA INDE CELL EDIAT LIBF CLON RES OTHE	THARA TH: THE	ACTER 543 uclei uclei y: li E: cl RCE: no RCE: Te JAL/I DURCE CDN 2.3	enebi [SOL# fat b	ICS: pai id ouble co mf	RNA moli: none and	who]	ed n S			inus	
	TTGT	TTAG	CGG A	ATGG/	AATT(CC C1	rc <i>g</i> t#	AGGGG	S ATA	AATTT	гтбт	TTA	TTT/	AAG	50
AAGG	SAGAT	ΓAT A					AGC (Ser H -					lis H			96
							AGC Ser								141
							TCC Ser								186
							GAA Glu 15								537
							GTC Val 30								276
							GTC Val 45								357
							GAC Asp 60								366
							AGC Ser 75								411
							AAG Lys 90								456
							TAC Tyr 105								501
		GAT Asp 115		СТС	SAGCA	ACC A	ACCA(CAC	IA CO	CACTO	SAGAT	Γ			543

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(2) INFORMATION FOR SEQ. ID NO: 23
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
- (ix)FEATURES
- (D) OTHER INFORMATION: Mature Protein with His-tag (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro -30 -25 -20
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5
- Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys 10
- Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val 15 20 25 30
- Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu 35 40 45
- Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60
- Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu 65 70 75
- Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu 80 90
- Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp 95 100 105 110
- Phe Ser Pro Ile Asp *

- (2) INFORMATION FOR SEQ. ID NO: 24
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix)FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -65 -60 -55	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -50 -45 -40	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile -35 -30 -25	186
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser -20 -15 -10	537
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile -5	276
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly 10 15 20	357
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu 25 30 35	366
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn 40 45 50	411
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu 55 60 65	456
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu 70 75 80	501
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu 85 95	546
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys 100 105 110	595
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG Phe Ser Pro Val Asp * 』35	643
TGTGCTTTAC ATATAAAAAT AAAGTGTTTC TGATGTAAAA AAAAAAAAA	693
AAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT	743
TCCACCCTC GAGCACCACC ACCACCACCA CTGAGAT	777

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(2) INFORMATION FOR SEQ. ID NO: 25
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
- (ix)FEATURES
- (D) OTHER INFORMATION: Precursor Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro -50
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg -35
- Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile
- Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
- Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val
- Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp
- Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu
- Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val
- Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys
- Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe 700
- Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp * 105 770 115

(5)		i) S ii) iii) iv) vi)	EQUEI (A) (B) (C) (D) MOLE HYP ANTI (A) (C) IMMI (A) (B) EATUI	NCE (LENG TYPI STR. TOPO CULE OTHE -SEN: INAL INAL CELI EDIA CLOI RES	CHAR, GTH: E: n; ANDE: OLOG' TYPI TICAI SE: I SOUI ANISI L TYPI TE S(RARY NE:]	ACTEI 543 ucle: UC	RIST: base ic ac S: dc inear DNA 1 D enebe E1SOLA fat b E: NA 7	ICS: pa: cid cuble to mh	RNA moli none and	e who:					
	()	xi):	(D) SEQUI	OTH	DES(NFORI CRIP	MATI(FION:	: ZE	His-	tagge NO:	26: 56₁;	Sign	al mi	inus	
															50
AAG	GAGA'	ΓΑΤ .				Ser S	Ser H				His H	His I			96
AGC Ser	GGC Gly	CTG Leu -20	GTG Val	CCG Pro	CGC Arg	GGC Gly	AGC Ser -15	CAT His	ATG Met	GCT Ala	AGC Ser	ATG Met -10	ACT Thr	GGT Gly	141
GGA Gly	CAG Gln	CAA Gln -5	ATG Met	GGT Gly	CGC Arg	GGC Gly	CTG Leu 1	ACC Thr	GAG Glu	GCA Ala	CAA Gln 5	ATT	GAG Glu	AAA Lys	186
CT6 Leu	AAC Asn 10	AAG Lys	ATC	Ser Ser	AAA Lys	AAA Lys 165	TGT Cys	CAA Gln	AAT Asn	GAA Glu	TDA Ser 20	GGA Gly	GTG Val	TCG Ser	537
															276
CCT Pro	AAA Lys 40	CTG Leu	AAA Lys	CGC Arg	CAA Gln	GTT Val 45	TTT Phe	TGC Cys	GTG Val	GCC Ala	AGG Arg 50	AAC Asn	GCC Ala	GGT Gly	357
CTG Leu	GCC Ala 55	ACG Thr	GAA Glu	TCG Ser	GGA Gly	GAG Glu LO	GTG Val	GTG Val	GTC Val	Asp	Val	TT6 Leu	AGG Arg	GAG Glu	366
															411
ATC Ile	AAT Asn 85	AAG Lys	TGC Cys	GCC Ala	GTC Val	AAG Lys 90	AGA Arg	GAT Asp	ACT Thr	GTT Val	GAA Glu 95	GAG Glu	ACG Thr	GTG Val	456
															501
				СТС	SAGC	ACC A	ACCA(CAC	IA C	CACTO	AGA"	Γ			543
	AAGC AGCY CTG Leu CAAAGIN CCT Pro CTG Leu AAG Lys ATC Ile TTC Phe CCA	AAGGAGA AAGGAGAGA AAGGAGAGA AAGGAGAGA AAGGAGAGA AAGGAGAGA CTG AAC Leu AAC Leu AAC Leu AAC Leu AAC CTG GCC Leu AC Leu AC CTG GCC Leu AC CTG GCC Leu AC CTG GCC Leu AC CTG GCC CT AAA CTC AAT CTC	(i) SI (iii) (iv) (iv) (vi) (vi) (vi) (vi) (vi)	(i) SEQUE (A) (B) (C) (ii) MOLE (iii) HYP (iv) ANTI (vi) ORIG (A) (B) (Vii) IMM (A) (B) (ix)FEATU (D) (xi) SEQUE TTGTTAGCGG AAGGAGATAT ACC AGC GGC CTG GTG Ser Gly Leu Val -20 GGA CAG CAA ATG Gly Gln Gln Met -5 CTG AAC AAG ATC Leu Asn Lys Ile L0 CAA GAG ATC ATA Glu Ile Ile 25 CCT AAA CTG AAA Pro Lys Leu Lys 40 CTG GCC ACG GAA Leu Ala Thr Glu S5 AAG GTG AGG AAG Lys Val Arg Lys 70 ATC AAT AAG TGC Ile Asn Lys Cys 85 TTC AAT AAG TGC Ile Asn Thr Phe L00 CCA GTT GAT TGA Pro Val Asp *	(i) SEQUENCE (A) LEN (B) TYP (C) STR (D) TOP (ii) MOLECULE (iii) HYPOTHE (iv) ANTI-SEN (vi) ORIGINAL (A) ORG (B) IND (C) CEL (vii) IMMEDIA (A) LIB (B) CLO (ix)FEATURES (D) OTH (xi) SEQUENCE TTGTTAGCGG ATGG AAGGAGATAT ACC ATG Met AGC GGC CTG GTG CCG Ser Gly Leu Val Pro -20 GGA CAG CAA ATG GGT Gly Gln Gln Met Gly -5 CTG AAC AAG ATC AGC Leu Asn Lys Ile Ser LO CAA GAG ATC ATA ACC Gln Glu Ile Ile Thr 25 CCT AAA CTG AAA CGC Pro Lys Leu Lys Arg 40 CTG GCC ACG GAA TCG Leu Ala Thr Glu Ser S5 AAG GTG AGG AAG GTC Lys Val Arg Lys Val 70 ATC AAT AAG TGC GCC Ile Asn Lys Cys Ala B5 TTC AAT ACT TTC AAA Phe Asn Thr Phe Lys LOC CCA GTT GAT TGA CTCC Pro Val Asp *	(i) SEQUENCE CHAR, (A) LENGTH: (B) TYPE: ni (C) STRANDE: (D) TOPOLOG (ii) MOLECULE TYPE (iii) HYPOTHETICAL (iv) ANTI-SENSE: Note of the content of th	(i) SEQUENCE CHARACTER (A) LENGTH: 543 (B) TYPE: nuclei (C) STRANDEDNESS (D) TOPOLOGY: 1: (ii) MOLECULE TYPE: c. (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: T. (B) INDIVIDUAL/ (C) CELL TYPE: (vii) IMMEDIATE SOURCE (A) LIBRARY: cDI (B) CLONE: 13-1: (ix)FEATURES (D) OTHER INFORM (xi) SEQUENCE DESCRIPT TTGTTAGCGG ATGGAATTCC CT AAGGAGATAT ACC ATG GGC AGC AGC AGC AGC AGC AGC AGC AGC AG	(i) SEQUENCE CHARACTERIST: (A) LENGTH: 543 bas (B) TYPE: nucleic a (C) STRANDEDNESS: d (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA ((iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Teneb. (B) INDIVIDUAL/ISOL. (C) CELL TYPE: fat b (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: l3-l7 (ix)FEATURES (D) OTHER INFORMATIC (xi) SEQUENCE DESCRIPTION: TTGTTAGCGG ATGGAATTCC CTCGT; AAGGAGATAT ACC ATG GGC AGC AGC AGC AGC AGC AGC AGC AGC AG	(i) SEQUENCE CHARACTERISTICS:	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio moli (B) INDIVIDUAL/ISOLATE: non (C) CELL TYPE: fat body and (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 13-17 (ix)FEATURES (D) OTHER INFORMATION: His- (xi) SEQUENCE DESCRIPTION: SEQ ID TTGTTAGCGG ATGGAATTCC CTCGTAGGGG AT. AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT AGC GAY CAT CAT GAY CAT	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INJIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and who: (vii) IMMEDIATE SOURCE: (A) LIBRARY: CDNA (B) CLONE: L3-L7 (ix)FEATURES (D) OTHER INFORMATION: His-taggs (xi) SEQUENCE DESCRIPTION: SEQ ID NO: TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATT AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT GET GIV Leu Val Pro Arg Gly Ser His Met Ala -15 GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA GGLY GIV GIV Arg Gly Leu Thr Glu Ala -5 CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu 10 CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC GIV Ile Ile Thr Lys Ala Arg Asn Gly Asp 25 CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala 40 CTG GCC ACG GAA TCG GGA GAG GAG GTG GTC GAC GAC ALA ARG TG CAC ALA ARG ATC ALA ACC AAA GAT TTT TGC GTG GCC CAC ALA ARG Leu Ala Thr Glu Ser Gly Glu Val Val Val Val Asp 40 CTG GCC ACG GAA TCG GGA GAC GAC GAC GAC GAC GAC GAC GAC G	(i) SEQUENCE CHARACTERISTICS:	(i) SEQUENCE CHARACTERISTICS:	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 13.17 (ix) FEATURES (D) OTHER INFORMATION: His-tagged, Signal mid (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26: TIGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTA AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AMET GIV SEQUENCE DESCRIPTION: SEQ ID NO: 26: TIGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTA AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AMET GIV Sep His His His His His His His Sequence Description: Seq ID No: 26: TIGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTA AAGGAGATAT ACC ATG GGC AGC CAT CAT CAT CAT CAC AMET GIV Sep His Het Ala Sep Met Thr -2D AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT Sep Gly Leu Val Pro Arg Gly Sep His Met Ala Sep Met Thr -2D GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG GIV Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu -5-5 CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val 1D CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GCC Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Thr Glu Ser Gly Glu Val Val Val Asp Trp Glu Asp 35 CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg 55 AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA CYS Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys 70 AAC GTG AAG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA CYS Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Slu Lys 70 AAC GTG AAG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAC AAC GTC AAT ACT TCC AAA TAT CTT CAAA TGT GTC ATG AAA AAC AAG CCA AAG TTC PAS AND Thr Ph	(i) SEQUENCE CHARACTERISTICS: (A) LENGHT: 5'12 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (Vi) IMMEDIATE SOURCE: (A) LIBRARY: CDNA (B) CLONE: 13-17 (ix)FEATURES (D) OTHER INFORMATION: His-tagged; Signal minus (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2b: TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAGG AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser -30 -25 AGC GGC CTG GTG CGC GGC GGC AGC CAT ATG GCT AGC ATG ACT GGT AGC AGC AGC AGC AGC AGC AGC AGA ATT GAG AAA Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys -5 L CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser Lo CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT GAT GAT CGT TGG GAG GAC GAT AGA AGT GIU Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp 30 CCT AAA CTG AAA CGC CAA GGT TTTT TGC GTG GCC AGG GAC GAT AGA GGY GAC GAT

- (2) INFORMATION FOR SEQ. ID NO: 27
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix)FEATURES
 - (D) OTHER INFORMATION: Mature Protein with His-tag (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -30 -25 -20
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -15 -10 -5
- Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys
 L
 5
 L0
 L5
- Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg 20 25 30
- Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys 35 40 45
- Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val 50 55 60
- Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu 65 70 75
- Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu 80 85 90 95
- Glu Thr Val Phe Asn Thr Phe Lys (ys Val Met Lys Asn Lys Pro Lys 100 105 110
- Phe Ser Pro Val Asp * 115

- (2) INFORMATION FOR SEQ. ID NO: 28
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

•	TTGT	TTAG	IGG ,	ATGG.	AATT	cc c	TCGT	AGGG	G AT	AATT	TTGT	TTA	сттт	AAG	50
AAGG	AGAT	ΓΑΤ /	، ۲۲ ا	ATG (Met (GGC / Gly :	Ser :	AGC Ser -55	CAT	CAT His	CAT His	His	CAT (His ! -50	CAC His	AGC Ser	96
AGC (GGC Gly	CTG Leu -45	GTG Val	CCG Pro	CGC Arg	GGC Gly	AGC Ser -40	CAT	ATG Met	GCT Ala	AGC Ser	ATG Met -35	ACT Thr	GGT Gly	141
GGA (Gly (CAG Gln	CAA Gln -30	ATG Met	GGT Gly	CGC Arg	GGA Gly	TCC Ser -25	GAA Glu	TTC Phe	GCA Ala	CGA Arg	GCA Ala -20	AAA Lys	ATG Met	186
AAA (Lys l	CTC Leu	CTC Leu -15	TTG Leu	TGC Cys	TTT Phe	GCT Ala	TTC Phe -10	GCC Ala	GCC Ala	ATC Ile	GTC Val	ATC Ile -5	GGA Gly	GCT Ala	531
CAG (GCT Ala	CTC Leu 1	ACC Thr	GAC Asp	GAA Glu	CAG Gln 5	ATA Ile	CAG Gln	AAA Lys	AGG Arg	AAC Asn 10	AAG Lys	ATC	AGC Ser	276
AAA (GAA Glu 15	TGC Cys	CAG Gln	CAG Gln	GTG Val	TCC Ser 20	GGA Gly	GTG Val	TCC Ser	CAA Gln	GAG Glu 25	ACG Thr	ATC Ile	GAC Asp	357
AAA (GTC Val 30	CGC Arg	ACA Thr	GGT Gly	GTC Val	TTG Leu 35	GTC Val	GAC Asp	GAT Asp	CCC Pro	AAA Lys 40	ATG Met	AAG Lys	AAG Lys	366
CAC 0	GTC Val 45	CTC Leu	TGC Cys	TTC Phe	TCG Ser	AAG Lys 50	AAA Lys	ACT Thr	GGA Gly	GTG Val	GCA Ala 55	ACC Thr	GAA Glu	GCC Ala	411
GGA 6 Gly A	GAC Asp 60	ACC Thr	AAT Asn	GTG Val	GAG Glu	GTA Val L5	CTC Leu	AAA Lys	GCC Ala	AAG Lys	CTG Leu 70	AAG Lys	CAT	GTG Val	456
GCC A	AGC Ser 75	GAC Asp	GAA Glu	GAG Glu	GTG Val	GAC Asp 80	AAG Lys	ATC	GTG Val	CAG Gln	AAG Lys 85	TGC Cys	GTG Val	GTC Val	501
AAG A															546
Ile 7	TAC Tyr 105	GAC Asp	TDA Ser	AAA Lys	CCT Pro	GAT Asp LLO	TTC Phe	TCT Ser	CCT Pro	ATT	GAT Asp 115	TAA *	TTG	TTTTGTA	595
TTTGA	ACTG	SAA T	TTTG	SACAA	AT AA	AAGGT	ΓΑСΤΑ	A TC	GTTA	TGTA	AAA	4444	AAA		645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT											681				

- (2) INFORMATION FOR SEQ. ID NO: 29
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30
- Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala -25 -20 -15
- Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile -10 -5 1 5
- Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
- Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35
- Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
- Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu 55 60 65 70
- Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys 75 80 85
- Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
 90 95 100
- Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 115

(2) INFORMATION FOR SEQ. ID NO: 30 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (v) (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 3.4 (ix) FEATURES (D) OTHER INFORMATION: His-tagged; Signal minus (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:	
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -30 -25	ЯЬ
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -20 -15 -10	141
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln -5	186
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val 10 15 20	531
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp 25 30 35	276
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr 40 45 50	357
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys 55 &BO &S	44E
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile 70 75 80	411
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala 85 90 95	456
TAT GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser 100 105 110	501
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT Pro Ile Asp *	543

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(2) INFORMATION FOR SEQ. ID NO: 31
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
- (ix) FEATURES
 - (D) OTHER INFORMATION: Mature Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys $^{\rm L}$

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp 95 100 105

- (2) INFORMATION FOR SEQ. ID NO: 32
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50								
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -55 -50	96								
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141								
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	186								
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -5	531								
CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser 1 10	276								
AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	357								
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366								
CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala 45 50 55	411								
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val LD L5 70	456								
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501								
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546								
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 115	595								
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAA 64									
AAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT									

- (2) INFORMATION FOR SEQ. ID NO: 33
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30
- Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala -25 -20 -15
- Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile -10 -5 1 5
- Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val
- Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35
- Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly Val 40 45 50
- Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu 55 60 65 70
- Lys HisVal Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys 75 80 85
- Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys 90 95 100
- Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 115 115

(2) INFORMATION FOR SEQ. ID NO: 34 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 3.9 (ix) FEATURES (D) OTHER INFORMATION: His-tagged, Signal minus (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:									
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50								
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -30 -25									
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GG Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gl -10 -15 -10									
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAT GAA CAG ATA CA Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gl -5 L 5									
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GT Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Va 10 15 20									
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GA Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val As 25 30 35									
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA AC Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Th 40 45 50									
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AA Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Ly 55 60 65									
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG AT Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Il 70 75 80									
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GC Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Al 85 90 95									
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TC Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Se 100 105 110									
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT Pro Ile Asp * 115	543								

- (2) INFORMATION FOR SEQ. ID NO: 35
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Mature Protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro -30 -25 -20
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -1.5 -10 -5
- Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
- Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val 15 20 25 30
- Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu 35 40 45
- Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60
- Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu 65 70 75
- Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu 80 85 90
- Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp 95 100 105
- Phe Ser Pro Ile Asp *

- (2) INFORMATION FOR SEQ. ID NO: 36
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

	ттс	TTAG	CGG .	ATGG.	ААТТ	cc c	TCGT.	AGGG	G AT	AATT	ттст	ТТА	C T TT	AAG	50
AAG	GAGA	TAT.			Gly :						CAT His -50				96
		Leu									AGC Ser -35	Met			141
GGA Gly	CAG Gln -30	CAA Gln	ATG Met	GGT Gly	CGC Arg	66A 61y -25	TCC Ser	GAA Glu	TTC Phe	GCA Ala	CGA Arg -20	GCA Ala	AAA Lys	ATG Met	186
											GTC Val -5				531
CAG Gln	GCT Ala L	CTC Leu	ACC Thr	GAC Asp	GAA Glu 5	CAG Gln	ATA Ile	CAG Gln	AAA Lys	AGG Arg	AAC Asn 10	AAG Lys	ATC	AGC Ser	276
AAA Lys	GAG Glu 15	TGC Cys	CAG Gln	CAG Gln	GTG Val	TCC Ser	GGA Gly	GTG Val	TCC Ser	CAA Gln	GAG Glu 25	ACG Thr	ATC Ile	GAC Asp	357
AAA Lys	GTC Val 30	CGC Arg	ACA Thr	GGT Gly	GTC Val	TTG Leu 35	GTC Val	GAC Asp	GAT Asp	CCC Pro	AAA Lys 40	AT <i>G</i> Met	AAG Lys	AAG Lys	366
CAC His	GTC Val 45	CTC Leu	TGC Cys	TTC Phe	TCG Ser	AAG Lys 50	AAA Lys	ACT Thr	GGA Gly	GTG Val	GCA Ala 55	ACC Thr	GAA Glu	GCC Ala	411
GGA Gly	GAC Asp LO	ACC Thr	AAT Asn	GTG Val	GAG Glu	GTA Val 65	CTC Leu	AAA Lys	GCC Ala	AAG Lys	CTG Leu 70	AAG Lys	CAT	GTG Val	456
											AAG Lys 85				501
AAG Lys	AAG Lys 90	GCC Ala	ACA Thr	CCA Pro	GAG Glu	GAA Glu 95	ACG Thr	GCT Ala	TAT Tyr	GAC Asp	ACC Thr 100	TTC Phe	AAG Lys	TGT Cys	546
ATT Ile	TAC Tyr 105	GAC Asp	AGT Ser	AAA Lys	CCT Pro	GAT Asp LLO	TTC Phe	TCT Ser	CCT Pro	ATT	GAT Asp 115	T A A *	TTG	TTTTGTA	595
TTTGGCTGAA TTTTGACAAT AAAGGTACTA TCGTTATGTA AAAAAAAAA										645					
		r.c.c			-, -										

681

AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT

- (2) INFORMATION FOR SEQ. ID NO: 37
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Precursor Protein with His-tag
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37
- Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 -55 -50 -45
- Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 -40 -35 -30
- Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala -25 -20 -15
- Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile -10 -5 1 5
- Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
- Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35
- Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val 40 45 50
- Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu 55 60 65 70
- Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys 75 80 85
- Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys 95 100
- Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 115

(2) INFORMATION FOR SEQ. ID NO: 38 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 543 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organ (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 7.5 (ix) FEATURES (D) OTHER INFORMATION: His-tagged Sign (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:	
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	CTTTAAG 50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT Met Gly Ser Ser His	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met -20 -15	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln -5 1	ATA CAG 186 Ile Gln
AAA AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser 10 15 20	GGA GTG 231 Gly Val
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu 25 30 35	GTC GAC 276 Val Asp
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys 40 45	AAA ACT 321 Lys Thr
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val 55 60	CTC AAA 366 Leu Lys
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp 70 75 80	AAG ATC 4ኔኔ Lys Ile
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu 85	ACG GCT 45b Thr Ala
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp 100	TTC TCT 501 Phe Ser
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT Pro Ile Asp * Ll5	543

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(2) INFORMATION FOR SEQ. ID NO: 39
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
- (ix) FEATURES
 - (D) OTHER INFORMATION: Mature protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys

5 10

Glu (ys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu 80 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp 95 100 105

Phe Ser Pro Ile Asp * LL5

- (2) INFORMATION FOR SEQ. ID NO: 40
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 12.84 upper primer with Bam-H1 site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGCGGATCCC TCACCGACGA ACAG

24

- (2) INFORMATION FOR SEQ. ID NO: 41
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 12.84 lower primer with Xhol site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAGGATAA CTAATTGAGC TCGCC

25

- (2) INFORMATION FOR SEQ. ID NO: 42 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (V)
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism

24

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
- (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 13.17 upper primer with Bam-H1 site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CGCGGATCCC TGACCGAGGC ACAA

- (2) INFORMATION FOR SEQ. ID NO: 43
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 13.17 lower primer with Xhol site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAGTGGTCAA CTAACTGAGC TCGCC

25

(2) INFORMATION FOR SEQ. ID NO: 44 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 481 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no											
<pre>(vi) ORIGINAL SOURCE:</pre>											
GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCN TTC GCC GCC Met Lys Leu Leu Cys Phe Ala Phe Ala Ala -15 -10	46										
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAY GAA CAG ATA CAG AAA Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys -5	71										
AGG AAC AAG ATC AGC AAA GAR TGC CAG CAG GNG TCC GGA GTG TCC Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser 10 15 20	736										
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAY GAT Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35	181										
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG ARA ACT GGA Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly 40 45 50	556										
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala 55 60	271										
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAR GTG GAC AAG ATC GTG Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val 70 75 80	316										
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr 85 90 95	361										
GAC ACC TTC AAG NNT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro 100 105 110	406										
ATT GAT TAA TTGTTTTGTA TTTGRCTGAA TTTTGACAAT AAAGGTANTA Ile Asp * 115	455										
TCGTTATGNA AAAAAAAA AAAAAA	481										

(2)	(i (i (i (v	i) M ii) M v) A vi) O	(B) (C) (D) OLECO NTI- RIGI (A) (C) IMME (A) (B)	CE C LENG TYPE STRA TOPO ULE THET SENS ORGA INDI CELL DIAT LIBR CLON	HARA TH: NDED LOGY TYPE ICAL E: UR NISM VIDU TYPE ARY: E: 2	CTER 481 clei NESS : li : cD c re CE: Te AL/I E: f URCE cDN .2	ISTI base c ac c do near NA t enebr SOLA at b	CS: pai id uble o mR io m TE: ody	NA colit none and	whol	e or			∶44 with	Tm 13.17
	(×	(i) S	EQUE									354		1. WION	
GGCA	NRNN	INN A	AR A	TG A let L	AR Y ys L	eu L	.eu L	'NN T .eu (GY Y ys F	TN R	YN T	YC N he A	IYC R	YY la	46
NTN Ile	NTN Val	RTC Ile -5	RNA Gly	GYT Ala	CAG Gln	GCY	CTN Leu 1	ACC Thr	GAN Asp	GNA Glu	CAR Gln 5	ATN	NAG Gln	AAA Lys	91
NNG Arg	AAC Asn 10	AAG Lys	ATC Ile	AGC Ser	AAA Lys	RAR Glu 15	TGY Cys	CAR Gln	NAN Gln	GNR Val	YNN Ser 20	GGA Gly	GTG Val	TCN Ser	136
CAA Gln	GAG Glu 25	AYN Thr	ATN Ile	RNC Asp	AAA Lys	GYY Val 30	CGC Arg	ANN Thr	GGT Gly	GNC Val	TNG Leu 35	GNN Val	GAY Asp	GAT Asp	181
CCY Pro	AAA Lys 40	NTG Met	AAR Lys	NRN Lys	CAN His	GTY Val 45	YTY Leu	TGC Cys	NTN Phe	NCN Ser	ARG Lys 50	ARN Lys	RCY Th r	GGN Gly	55P
											GTR Val L 5				271
											RYN Val 80				316
RTN Val	NAN Gln 85	AAG Lys	TGC Cys	GYN Val	GTC Val	AAG Lys 90	ARR Lys	GNY Ala	ACN Thr	NYN Pro	GAR Glu 95	GAR Glu	ACG Thr	GYN Ala	367
											CCN Pro 110				406
		GAT Asp		NYNI	INYYN	NNA '	YTNG	NNNR	NR N	TTYR	ANAA1	Г АА.	AGNNI	NNTN	458
TNR	TNNN	RNA .	AAAA.	AAA A	AA A	AAAA	A								484

(2) INFORMATION FOR SEQ. ID NO: 46 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 481 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA (iii) HYPOTHETICAL: no (iv) ANTI-SENSE: no (v) (vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 2.2 (ix) FEATURES (D) OTHER INFORMATION: Concensus of Seq ID #45 with B1/B2 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:									
GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYY NYC RYY 46 Met Lys Leu Leu Cys Phe Ala Phe Ala Ala -15 -10									
NTN NTN RTC NNA GYT CAG GCY NTN ACY NAN GNA NAN NTN NAG NNA Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys -5	91								
NNG NNC NAR AYC AGC RNA RAR TGY NAR NNN GNR NNY GGA GTG TCN Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser LO L5	136								
NAA GAN RYN ATN RNN ARA GYY CGC ANN GGT GNC TNG GNN GAY GAY Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30	181								
CCY AAA NTG AAR NNN CAN NTY YTY TGC NTN NYN ARG RNN NYY GRN Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly 4D 45 50	556								
NTR GYN RCN GAA NCN GGA GAN RYN RNN GYN GAN RYR YTN ARR GNN Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala 55	271								
AAG NTG ANG NRN NNN NNN RNN ANN RNN RAR RAR RYN RRN ARR NTN Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile 70 75 80	376								
NYN NRN ARN NNN NNN NNN NNG ARN RNN NYN NNN RAR RNR NNN NNN Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala 85 90	367								
TNN RAN NYN YYN AAN NNN NNY NNN RRN ANN ARN CCN RNN TYY TYN Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser 100 1505	406								
CNN RYT RNT TRN NYNNNNNNN YNNGNNNRNR NTTYRANAAT AAAGNNNYTN Pro Ile Asp * 115	458								
TNRTNNNRNA AAAAAAAAA AAAAAA	484								

(2)	(i (i	i) SE	QUEN (A) (B) (C) (D) 10LEC HYPC	ICE C LENG TYPE STRA TOPC ULE THET	HARA TH: NDED LOGY TYPE LICAL SE: r	CTER 48L IClei NESS ': li : cI : cI	RIZII base c ac c do near	CS: pai id ouble	2						
	<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Tenebrio molitor (B) INDIVIDUAL/ISOLATE: none (C) CELL TYPE: fat body and whole organism (vii) IMMEDIATE SOURCE: (A) LIBRARY: cDNA (B) CLONE: 2.2 (ix) FEATURES (D) OTHER INFORMATION: Concensus of Seq. ID #46 with AFP-3 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:</pre>														
GGC	NNRNI	INN A		ATG A 1et l		.eu l					la F				46
	NTN Val														71
	NNY Asn 10														136
	GAN Glu 25														181
	AAA Lys 40														556
	RYN Ala 55														271
	NTN Leu 70														37.6
	NNN Gln 85														367
	RAN Asp 100														406
	NYN Ile 115			NNN	NNNNI	NNN	YNNR	NNNN	NN NI	NNNNI	NN A A '	Γ ΑΑ,	ANNNI	NNNN	45 8

484

NNNNNNNA AAAAAAAA AAAAA

- (2) INFORMATION FOR SEQ. ID NO: 48
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 Amino Acids
 - (B) TYPE: Amino Acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: Protein
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Tenebrio molitor
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE:
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Genral Concensus of Clones, BL, B2 and AFP-3

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
                        Leu Ile Ser Leu Ile Leu Leu Val Thr Val
                Cys
                            Thr Leu Val
                                                     Ala Ala Thr
                            Val
                                                     -5
            -15
                                 -10
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
        Ile Glu Ala Asp Leu Glu Leu Leu Arg Gln Thr
                                                             Ala
                    Thr Pro Arg
                                             Lys
                                                     His
                                                             Asp
Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
                                    Glu Asp Ile Leu Thr Arg Ala
                            Ala
       Lys Asn Val
                                         Ala Val
            Thr
                                                     Lys
Ala
                                             Ser
                                                     Asn
            Ala
                                                              30
                    20
15
Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
                                                 Arg Gln Leu Phe
                                         Leu
    Asn Arg Asp Trp Glu
                                                 Met
                                                         Ala
            Glu Glu
                                                 Glu
                                                          45
                                     40
                35
Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
    Val Ala Arg Arg Ala Ile Leu Val Ala Ala Ser
                                                     Glu Ile Glu
                Ala Leu Glu Ile Ile Asp
                                                          Val Val
    Ile Phe
                             Glu
                                                         Phe Gln
        Leu
                Asn
                             Phe
                                 55
                                                     PO
            50
Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser ^^^ Asp Glu
                             Val Thr Arg Asn Thr Asn Asp Pro
Ala Asp Thr Phe Arg Glu
                                             Ser Asp Asn
                             Phe Arg Lys
        His Ile
                    Thr
                                     Glu
                                                 Glu His
                             70
                                                 75
        Ь5
Glu Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro
Lys Ser Glu Asp Leu Ile Glu
                                     Ala
                                             Thr Glu Asp
                         Asn
                                     Thr
                                                 Arg
    Thr
                         Ala
                                             90
    80
                         85
Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro
Gln Asp Ser Val Phe Glu Val Thr
                                   Val Val Leu Lys Asn Arg Ser
                                             Met
            Ser Ala Asn Phe
                                                      Asp
    His
                                             His
                                         105
                                                              110
95
                     700
Asp Phe Ser Pro Ile Asp ^^^ *
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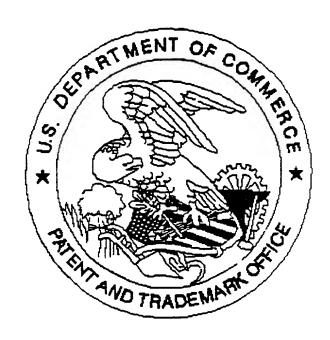
Phe Gly Asp Leu Phe Val *

Val 115

Asn Lys

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